

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/577,775
Source: JFWD
Date Processed by STIC: 05/11/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/577,775</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules.	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/577,775

DATE: 05/11/2006
TIME: 11:21:12

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\05112006\J577775.raw

3 <110> APPLICANT: KIM, TAE-YOON
4 BIO CLUE & SOLUTION CO., LT
6 <120> TITLE OF INVENTION: EC SOD and Cell transducing EC SOD and use thereof
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/577,775
C--> 8 <141> CURRENT FILING DATE: 2006-04-28
W--> 0 <130> FILE REFERENCE:
8 <150> PRIOR APPLICATION NUMBER: KR10-2003-0076629
9 <151> PRIOR FILING DATE: 2003-10-31
11 <160> NUMBER OF SEQ ID NOS: 33
13 <170> SOFTWARE: KopatentIn 1.71

Does Not Comply
Corrected Diskette Needed
(pg-1,2,3)

ERRORED SEQUENCES

479 <210> SEQ ID NO: 22 → 243 OK
480 <211> LENGTH: 243
481 <212> TYPE: PRT
482 <213> ORGANISM: Artificial Sequence
484 <220> FEATURE:
485 <223> OTHER INFORMATION: PEP1-EC SOD
488 <400> SEQUENCE: 22
489 Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
E--> 490 121 1265 12110 12615
491 Lys Lys Arg Lys Val Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser
E--> 492 14120 14025 15130
493 Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile
E--> 494 1565 16140 16645
495 Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly Thr Leu His Ala
E--> 496 17150 17655 18160
497 Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg
E--> 498 18665 19170 19675 20180
499 Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu
E--> 500 20685 21190 21695
501 Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser
E--> 502 221100 226101 231102
503 Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys
E--> 504 238110 241115 246120
505 Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln
E--> 506 251125 256130 261135
507 His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp
E--> 508 266140 271145 276150 281155
509 Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile
E--> 510 286160 291165 296170

Invalid Response. What is the source of genetic material. Pls see Glenn # Error Summary Sheet.

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Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\05112006\J577775.raw

511 Val Gly Arg Ala Val Val His Ala Gly Glu Asp Asp Leu Gly Arg
E--> 512 ~~301 175~~ ~~306 180~~ ~~311 185~~
513 Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu
E--> 514 ~~316 190~~ ~~321 200~~ ~~326 205~~
515 Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln
E--> 516 ~~331 210~~ ~~336 215~~ ~~341 220~~
517 Ala Arg Glu His Ser Glu Arg Lys Lys Arg Arg Glu Ser Glu Cys
E--> 518 ~~346 225~~ ~~351 230~~ ~~356 235~~ ~~361 240~~
519 Lys Ala Ala
523 <210> SEQ ID NO: 23
524 <211> LENGTH: 230
525 <212> TYPE: PRT
526 <213> ORGANISM: Artificial Sequence
528 <220> FEATURE:
529 <223> OTHER INFORMATION: PEP1-deltaHD/EC SOD
532 <400> SEQUENCE: 23
533 Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
E--> 534 ~~(123) 1~~ ~~(127) 5~~ ~~(32) 10~~ ~~(137) 15~~
535 Lys Lys Arg Lys Val Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser
E--> 536 142 147 152
537 Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile
E--> 538 157 162 167
539 Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly Thr Leu His Ala
E--> 540 172 177 182
541 Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg
E--> 542 187 192 197 202
543 Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu
E--> 544 207 212 217
545 Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser
E--> 546 222 227 232
547 Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys
E--> 548 237 242 247
550 Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln
E--> 551 252 257 262
552 His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp
E--> 553 267 272 277 282
554 Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile
E--> 555 287 292 297
556 Val Gly Arg Ala Val Val His Ala Gly Glu Asp Asp Leu Gly Arg
E--> 557 302 307 312
558 Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu
E--> 559 317 322 327
560 Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln
E--> 561 332 337 342
562 Ala Arg Glu His Ser Glu
E--> 563 347 352
706 <210> SEQ ID NO: 33
707 <211> LENGTH: 20
708 <212> TYPE: DNA

invalid
amino acid
numbers

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/577,775

DATE: 05/11/2006

TIME: 11:21:12

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577775.raw

709 <213> ORGANISM: Artificial Sequence

711 <220> FEATURE:

712 <223> OTHER INFORMATION: primer

715 <400> SEQUENCE: 33

716 tccaccaccc tgttgtgta

E--> 722 20 20

A handwritten note with a circled 'X' and an arrow pointing to it with the word 'delete' written next to it.

VERIFICATION SUMMARY

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,775

TIME: 11:21:13

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577775.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:490 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:492 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:494 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:496 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:498 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:502 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:504 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:506 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:508 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:510 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:512 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:514 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:516 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:518 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:534 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:536 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:538 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:540 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:546 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:548 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:551 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:555 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:557 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:559 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:561 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:563 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:722 M:254 E: No. of Bases conflict, this line has no nucleotides.